

SEQUENCE LISTING

<110> Powers, Scott
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Cutler, Gene
Tularik Inc.

<120> Novel G-Protein Coupled Receptors

<130> 018781-004730US

<140> US Not yet assigned
<141> Not yet assigned

<150> US 09/524,730
<151> 2000-03-14

<150> US 09/546,986
<151> 2001-04-11

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<170> PatentIn Ver. 2.1

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Pro Lys Ala Phe Ile Leu Leu Gly Val Ser Asp Arg Pro Trp Leu Glu
10 15 20

ctc cct ctc ttt gtg gtc ctc ctg ctg tcc tat gtg ctg gcc atg ttg 152
Leu Pro Leu Phe Val Val Leu Leu Ser Tyr Val Leu Ala Met Leu
25 30 35

ggg aac gtc gcc atc atc ctg gca tcc cgg gtg gat cct caa ctc cac 200
Gly Asn Val Ala Ile Ile Leu Ala Ser Arg Val Asp Pro Gln Leu His
40 45 50

agc ccc atg tac atc ttc ctc agt cac ctg tcc ttc ctg gac ctc tgc 248
Ser Pro Met Tyr Ile Phe Leu Ser His Leu Ser Phe Leu Asp Leu Cys
55 60 65

tac acc acc acg aca gtc cct cag atg ctg gtc aac atg ggc agt tcc 296
Tyr Thr Thr Thr Val Pro Gln Met Leu Val Asn Met Gly Ser Ser
70 75 80 85

cag aag acc atc agc tat gga ggc tgc act gtg caa tat gca gtc ttc Gln Lys Thr Ile Ser Tyr Gly Gly Cys Thr Val Gln Tyr Ala Val Phe 90 95 100	344
cac tgg ctg gga tgc acg gag tgc atc gtc ctg gcc gcc atg gcc ctg His Trp Leu Gly Cys Thr Glu Cys Ile Val Leu Ala Ala Met Ala Leu 105 110 115	392
gac cgc tac gtg gcc agc tgc aag ccc ctg cac tat gcc gtt ctc atg Asp Arg Tyr Val Ala Ser Cys Lys Pro Leu His Tyr Ala Val Leu Met 120 125 130	440
cac cgt gct ctc tgt cag cag ctc gtg gct ctg gcc tgg ctc agt ggc His Arg Ala Leu Cys Gln Gln Leu Val Ala Leu Ala Trp Leu Ser Gly 135 140 145	488
ttc ggc aac tcc ttc gtg cag gtg gtc ctg acg gtg caa ttg cca ttc Phe Gly Asn Ser Phe Val Gln Val Val Leu Thr Val Gln Leu Pro Phe 150 155 160 165	536
tgc ggg cgg cag gtg ctg aac aac ttt ttc tgt gag gtg ccc gcc gtg Cys Gly Arg Gln Val Leu Asn Asn Phe Phe Cys Glu Val Pro Ala Val 170 175 180	584
atc aag ctg tcg tgt gct gac acc gct atg aat gac acc ata ctg gct Ile Lys Leu Ser Cys Ala Asp Thr Ala Met Asn Asp Thr Ile Leu Ala 185 190 195	632
gtg ctg gtg gcc ttc ttc gtg ttg gtg ccc ctg gct ctc atc ctt ctc Val Leu Val Ala Phe Phe Val Leu Val Pro Leu Ala Leu Ile Leu Leu 200 205 210	680
tcc tat ggc ttt att gcc cgg gca gtg ctc agg atc cag tcc tcc aag Ser Tyr Gly Phe Ile Ala Arg Ala Val Leu Arg Ile Gln Ser Ser Lys 215 220 225	728
gga cga cac aag gcc ttt ggg acg tgt tcc tcc cac ctg atg atc gtc Gly Arg His Lys Ala Phe Gly Thr Cys Ser Ser His Leu Met Ile Val 230 235 240 245	776
tcc ctc ttc tac cta cct gcg att tac atg tat ctg cag ccc cct tcc Ser Leu Phe Tyr Leu Pro Ala Ile Tyr Met Tyr Leu Gln Pro Pro Ser 250 255 260	824
agc tac tcc caa gag cag ggc aaa ttt att tct ctc ttc tat tcc ata Ser Tyr Ser Gln Glu Gln Gly Lys Phe Ile Ser Leu Phe Tyr Ser Ile 265 270 275	872
atc acc ccc act ctc aat ccc ttc acc tac acc ctg aga aat aaa gat Ile Thr Pro Thr Leu Asn Pro Phe Thr Tyr Thr Leu Arg Asn Lys Asp 280 285 290	920
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Val	Leu	Ala	Met	Leu	Gly	Asn	Val	Ala	Ile	Ile	Leu	Ala	Ser	Arg	Val	
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Phe	Leu	Asp	Leu	Cys	Tyr	Thr	Thr	Thr	Val	Pro	Gln	Met	Leu	Val		
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Gln	Tyr	Ala	Val	Phe	His	Trp	Leu	Gly	Cys	Thr	Glu	Cys	Ile	Val	Leu	
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Ala	Trp	Leu	Ser	Gly	Phe	Gly	Asn	Ser	Phe	Val	Gln	Val	Val	Leu	Thr	
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Val	Gln	Leu	Pro	Phe	Cys	Gly	Arg	Gln	Val	Leu	Asn	Asn	Phe	Phe	Cys	
									165	170				175		
Glu	Val	Pro	Ala	Val	Ile	Lys	Leu	Ser	Cys	Ala	Asp	Thr	Ala	Met	Asn	
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Asp	Thr	Ile	Leu	Ala	Val	Leu	Val	Ala	Phe	Phe	Val	Leu	Val	Pro	Leu	
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Ala	Leu	Ile	Leu	Leu	Ser	Tyr	Gly	Phe	Ile	Ala	Arg	Ala	Val	Leu	Arg	
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Ile	Gln	Ser	Ser	Lys	Gly	Arg	His	Lys	Ala	Phe	Gly	Thr	Cys	Ser	Ser	
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His	Leu	Met	Ile	Val	Ser	Leu	Phe	Tyr	Leu	Pro	Ala	Ile	Tyr	Met	Tyr	
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Leu	Gln	Pro	Pro	Ser	Ser	Tyr	Ser	Gln	Glu	Gln	Gly	Lys	Phe	Ile	Ser	
									260	265				270		
Leu	Phe	Tyr	Ser	Ile	Ile	Thr	Pro	Thr	Leu	Asn	Pro	Phe	Thr	Tyr	Thr	
									275	280				285		
Leu	Arg	Asn	Lys	Asp	Met	Lys	Gly	Ala	Leu	Arg	Arg	Leu	Leu	Ala	Arg	
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 atg gga aag gac aat gcc agt tac cta cag gca ttc atc ctg gtg ggc 165
 Met Gly Lys Asp Asn Ala Ser Tyr Leu Gln Ala Phe Ile Leu Val Gly
 1 5 10 15

tct tct gat cgg cct gga ctg gag aaa att ctc ttt gct gtt atc ttg 213
 Ser Ser Asp Arg Pro Gly Leu Glu Lys Ile Leu Phe Ala Val Ile Leu
 20 25 30

atc ttc tgc atc ctg acc ctg gtg ggc aac act gcc atc atc ctc ttg 261
 Ile Phe Cys Ile Leu Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Leu
 35 40 45

ctg gtc atg gat gtc agg ctc cac aca ccc atg tac ttc ttt ctt ggg 309
 Leu Val Met Asp Val Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60

aat ctg tct ttc tta gat ctc tgc ttt aca gca agc att gcc cct cag 357
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
 65 70 75 80

ctg ctg tgg aac ctg ggg ggt cca gag aag acc atc acc tac cac ggc 405
 Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
 85 90 95

tgt gtg gcc caa ctc tac atc tac atg atg ctg ggc tcc acc gag tgc 453
 Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
 100 105 110

gtc ctc ctg gtt gtc atg tcc cat gac cgc tat gtg gcc gtc tgc cgg 501
 Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
 115 120 125

tcc ctg cac tac atg gca gtc atg cgc cca cat ctc tgc ctg cag ctg 549
 Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
 130 135 140

gtg act gtg gcc tgg tgc tgt ggc ttc cta aac tcc ttc atc atg tgt 597
 Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
 145 150 155 160

cct cag acg atg cag ctc cgg tgt gga cgt cgc agg gtg gac cac 645
 Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
 165 170 175

ttc ctg tgt gag atg cct gct ctt att gcc atg tct tgt gag gaa acc 693
 Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
 180 185 190

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Met Leu Val Glu Ala Ile His Leu Cys Pro Gly Gly Ser Pro Pro	
195 200 205	
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Gly Ala Ala Leu Pro His Pro His Leu Tyr Gly Val Ile Ala Ala Ala	
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gtg ctg agg atg aag tca gca gca ggg cga aag aaa gcc ttc cac acc	837
Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr	
225 230 235 240	
tgc tct tct cac ctc aca gtg gtc tct ctc ttc tac gga acc atc atc	885
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ile Ile	
245 250 255	
tac gtg tac ctg aag ccg gcc aac agc tac tcc caa gat cag ggg aag	933
Tyr Val Tyr Leu Lys Pro Ala Asn Ser Tyr Ser Gln Asp Gln Gly Lys	
260 265 270	
ttc ctg act ctc ttc tac acc atc gtc att ccc agc atc aac ccc ctc	981
Phe Leu Thr Leu Phe Tyr Thr Ile Val Ile Pro Ser Ile Asn Pro Leu	
275 280 285	
atc tac act ttg agg aac aag gat gtg aag ggg acc atg aag aaa ctt	1029
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Thr Met Lys Lys Leu	
290 295 300	
ctg ggg tgg gag aaa ggg gct ggg gag cct caa cga ggg gaa cac tct	1077
Leu Gly Trp Glu Lys Gly Ala Gly Glu Pro Gln Arg Gly Glu His Ser	
305 310 315 320	
agt aat gta gac agt ttg ctg gag tta ctc tct tag atgtgtctgt	1123
Ser Asn Val Asp Ser Leu Leu Glu Leu Leu Ser	
325 330	
ggccatgtgg agaactaata ttcaaggagt agagtgaacg cgggtggaa aatgcttcg	1183
agtttacccc cgtcctctgc cctctggatg tgaagtggtt tccttctgtt tgaagttgcc	1243
tgcttcagga tatctctgct gtatcttgca ctttccttgt cttttgatt tatccacaac	1303
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Ser Ser Asp Arg Pro Gly Leu Glu Lys Ile Leu Phe Ala Val Ile Leu	
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Ile Phe Cys Ile Leu Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Leu
 35 40 45
 Leu Val Met Asp Val Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
 65 70 75 80
 Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
 85 90 95
 Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
 100 105 110
 Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
 115 120 125
 Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
 130 135 140
 Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
 145 150 155 160
 Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
 165 170 175
 Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
 180 185 190
 Met Leu Val Glu Ala Ile His Leu Cys Pro Gly Gly Ser Pro Pro
 195 200 205
 Gly Ala Ala Leu Pro His Pro His Leu Tyr Gly Val Ile Ala Ala Ala
 210 215 220
 Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr
 225 230 235 240
 Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245 250 255
 Tyr Val Tyr Leu Lys Pro Ala Asn Ser Tyr Ser Gln Asp Gln Gly Lys
 260 265 270
 Phe Leu Thr Leu Phe Tyr Thr Ile Val Ile Pro Ser Ile Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Thr Met Lys Lys Leu
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 Leu Gly Trp Glu Lys Gly Ala Gly Glu Pro Gln Arg Gly Glu His Ser
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 Ser Asn Val Asp Ser Leu Leu Glu Leu Leu Ser
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aactgatgta attgcttcat gtctc atg ccc tgt atg ccc tgt gct ctt ccc 112
 Met Pro Cys Met Pro Cys Ala Leu Pro
 1 5

aca ggt ggc ctt ttg ccc cac ccc cag cat aca atg atg gaa ata gcc 160
 Thr Gly Gly Leu Leu Pro His Pro Gln His Thr Met Met Glu Ile Ala
 10 15 20 25

aat gtg agt tct cca gaa gtc ttt gtc ctc ctg ggc ttc tcc gca cga	30	35	40	208
Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu Gly Phe Ser Ala Arg				
ccc tca cta gaa act gtc ctc ttc ata gtt gtc ttg agt ttt tac atg	45	50	55	256
Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val Leu Ser Phe Tyr Met				
gta tcg atc ttg ggc aat ggc atc atc att ctg gtc tcc cat aca gat	60	65	70	304
Val Ser Ile Leu Gly Asn Gly Ile Ile Leu Val Ser His Thr Asp				
gtg cac ctc cac aca cct atg tac ttc ttt ctt gcc aac ctc tcc ttc	75	80	85	352
Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe				
ctg gac atg agc ttc acc acg agc att gtc cca cag ctc ctg gct aac	90	95	100	400
Leu Asp Met Ser Phe Thr Ser Ile Val Pro Gln Leu Leu Ala Asn				
ctc tgg gga cca cag aaa acc ata agc tat gga ggg tgt gtg gtc cag	110	115	120	448
Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly Cys Val Val Gln				
ttc tat atc tcc cat tgg ctg ggg gca acc gag tgt gtc ctg ctg gcc	125	130	135	496
Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys Val Leu Leu Ala				
acc atg tcc tat gac cgc tac gct gcc atc tgc agg cca ctc cat tac	140	145	150	544
Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg Pro Leu His Tyr				
act gtc att atg cat cca cag ctt tgc ctt ggg cta gct ttg gcc tcc	155	160	165	592
Thr Val Ile Met His Pro Gln Leu Cys Leu Gly Leu Ala Leu Ala Ser				
tgg ctg ggg ggt ctg acc acc agc atg gtg ggc tcc acg ctc acc atg	170	175	180	640
Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser Thr Leu Thr Met				
ctc cta ccg ctg tgt ggg aac aat tgc atc gac cac ttc ttt tgc gag	190	195	200	688
Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His Phe Phe Cys Glu				
atg ccc ctc att atg caa ctg gct tgt gtg gat acc agc ctc aat gag	205	210	215	736
Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu				
atg gag atg tac ctg gcc agc ttt gtc ttt gtt gtc ctg cct ctg ggg	220	225	230	784
Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly				
ctc atc ctg gtc tct tac ggc cac att gcc cgg gcc gtg ttg aag atc	235	240	245	832
Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala Val Leu Lys Ile				
agg tca gca gaa ggg cgg aga aag gca ttc aac acc tgt tct tcc cac	250	255	260	880
Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Ser His				

gtg gct gtg gtg tct ctg ttt tac ggg agc atc atc ttc atg tat ctc 928
Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile Phe Met Tyr Leu
270 275 280

cag cca gcc aag agc acc tcc cat gag cag ggc aag ttc ata gct ctg 976
Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys Phe Ile Ala Leu
285 290 295

ttc tac acc gta gtc act cct gcg ttg aac cca ctt att tac acc ctg 1024
Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu
300 305 310

agg aac acg gag gtg aag agc gcc ctc cgg cac atg gta tta gag aac 1072
Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His Met Val Leu Glu Asn
315 320 325

tgc tgt ggc tct gca ggc aag ctg gcg caa att tag agactccagt 1118
Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
330 335 340

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ttgggatgtc gttttcttc taatattgtt tgagctcaag gtagatggaa atctgaaagg 1238

agtgtgctca tgccatttcc agaccaagaa aacacattta ttatggcta attatcatag 1298

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receptor 3-A (BCA-GPCR-3-A)

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35 40 45

Phe Ile Val Val Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly
50 55 60

Ile Ile Ile Leu Val Ser His Thr Asp Val His Leu His Thr Pro Met
65 70 75 80

Tyr Phe Phe Leu Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr
85 90 95

Ser Ile Val Pro Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr
100 105 110

Ile Ser Tyr Gly Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu
115 120 125

Gly Ala Thr Glu Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr
130 135 140

Ala Ala Ile Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln
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Leu Cys Leu Gly Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr
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receptor 4 (BCA-GPCR-4)

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Ser Leu Gly Glu His Thr Leu His Met Gly Met Val Arg His Thr Asn
 10                      15                      20                      25

gag agc aac cta gca ggt ttc atc ctt tta ggg ttt tct gat tat gct      148
Glu Ser Asn Leu Ala Gly Phe Ile Leu Leu Gly Phe Ser Asp Tyr Ala
 30                      35                      40

cag tta cag aag gtt cta ttt gtg ctc ata ttg att ctg tat tta cta      196
Gln Leu Gln Lys Val Leu Phe Val Leu Ile Leu Ile Leu Tyr Leu Leu
 45                      50                      55

act att ttg ggg aat acc acc atc att ctg gtt tct cgt ctg gaa ccc      244
Thr Ile Leu Gly Asn Thr Thr Ile Ile Leu Val Ser Arg Leu Glu Pro
 60                      65                      70

aag ctt cat atg ccg atg tat ttc ttc ctt tct cat ctc tcc ttc ctg      292
Lys Leu His Met Pro Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu
 75                      80                      85

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95																
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Trp	Glu	Pro	Met	Lys	Thr	Ile	Ala	Tyr	Gly	Gly	Cys	Leu	Val	His	Leu	
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115																
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Tyr	Asn	Ser	His	Ala	Leu	Gly	Ser	Thr	Glu	Cys	Val	Leu	Pro	Ala	Leu	
125															135	
130																
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Met	Ser	Cys	Asp	Arg	Tyr	Val	Ala	Val	Cys	Arg	Pro	Leu	His	Tyr	Thr	
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145																
gtc	tta	atg	cat	atc	cat	ctc	tgc	atg	gcc	ttg	gca	tct	atg	gca	tgg	532
Val	Leu	Met	His	Ile	His	Leu	Cys	Met	Ala	Leu	Ala	Ser	Met	Ala	Trp	
155															165	
160																
ctc	agt	gga	ata	gcc	acc	acc	ctg	gta	cag	tcc	acc	ctc	acc	ctg	cag	580
Leu	Ser	Gly	Ile	Ala	Thr	Thr	Leu	Val	Gln	Ser	Thr	Leu	Thr	Leu	Gln	
170															185	
175																
ctg	ccc	tcc	tgt	ggg	cat	cgc	caa	gtg	gat	cat	tcc	atc	tgc	gag	gtc	628
Leu	Pro	Phe	Cys	Gly	His	Arg	Gln	Val	Asp	His	Phe	Ile	Cys	Glu	Val	
190															200	
195																
cct	gtg	ctc	atc	aag	ctg	gct	tgt	gtg	ggc	acc	acg	ttt	aac	gag	gct	676
Pro	Val	Leu	Ile	Lys	Leu	Ala	Cys	Val	Gly	Thr	Thr	Phe	Asn	Glu	Ala	
205															215	
210																
gag	ctt	ttt	gtg	gct	agt	atc	ctt	ttc	ctt	ata	gtg	cct	gtc	tca	ttc	724
Glu	Leu	Phe	Val	Ala	Ser	Ile	Leu	Phe	Leu	Ile	Val	Pro	Val	Ser	Phe	
220															230	
225																
atc	ctg	gtc	tcc	tct	ggc	tac	att	gcc	cac	gca	gtg	ttg	agg	att	aag	772
Ile	Leu	Val	Ser	Ser	Gly	Tyr	Ile	Ala	His	Ala	Val	Leu	Arg	Ile	Lys	
235															245	
240																
tca	gct	acc	ggg	aga	cag	aaa	gca	tcc	ggg	acc	tgc	ttc	tcc	cac	ctg	820
Ser	Ala	Thr	Gly	Arg	Gln	Lys	Ala	Phe	Gly	Thr	Cys	Phe	Ser	His	Leu	
250															265	
255																
aca	gtg	gtc	acc	atc	ttt	tat	gga	acc	atc	atc	ttc	atg	tat	ctg	cag	868
Thr	Val	Val	Thr	Ile	Phe	Tyr	Gly	Thr	Ile	Ile	Phe	Met	Tyr	Leu	Gln	
270															280	
275																
cca	gcc	aag	agt	aga	tcc	agg	gac	cag	ggc	aag	ttt	gtt	tct	ctc	ttc	916
Pro	Ala	Lys	Ser	Arg	Ser	Arg	Asp	Gln	Gly	Lys	Phe	Val	Ser	Leu	Phe	
285															295	
290																
tac	act	gtg	gta	acc	cgc	atg	ctt	aac	cct	ctt	att	tat	acc	ttg	agg	964
Tyr	Thr	Val	Val	Thr	Arg	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	
300															310	
305																
atc	aag	gag	gtg	aaa	ggg	gca	tta	aag	aaa	gtt	cta	gca	aag	gct	ctg	1012
Ile	Lys	Glu	Val	Lys	Gly	Ala	Leu	Lys	Lys	Val	Leu	Ala	Lys	Ala	Leu	
315															325	
320																

gga gta aat att tta tga ttataaaaaa aaaatttaag tgacactgtg atgaa 1065
Gly Val Asn Ile Leu
330 335

<210> 8
<211> 334
<212> PRT
<213> Homo sapiens

<220>
<223> human breast cancer amplified G-protein coupled
receptor 4 (BCA-GPCR-4)

<400> 8
Met Cys Tyr Leu Ser Gln Leu Cys Leu Ser Leu Gly Glu His Thr Leu
1 5 10 15
His Met Gly Met Val Arg His Thr Asn Glu Ser Asn Leu Ala Gly Phe
20 25 30
Ile Leu Leu Gly Phe Ser Asp Tyr Ala Gln Leu Gln Lys Val Leu Phe
35 40 45
Val Leu Ile Leu Ile Leu Tyr Leu Leu Thr Ile Leu Gly Asn Thr Thr
50 55 60
Ile Ile Leu Val Ser Arg Leu Glu Pro Lys Leu His Met Pro Met Tyr
65 70 75 80
Phe Phe Leu Ser His Leu Ser Phe Leu Tyr Arg Cys Phe Thr Ser Ser
85 90 95
Val Ile Pro Gln Leu Leu Val Asn Leu Trp Glu Pro Met Lys Thr Ile
100 105 110
Ala Tyr Gly Gly Cys Leu Val His Leu Tyr Asn Ser His Ala Leu Gly
115 120 125
Ser Thr Glu Cys Val Leu Pro Ala Leu Met Ser Cys Asp Arg Tyr Val
130 135 140
Ala Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Ile His Leu
145 150 155 160
Cys Met Ala Leu Ala Ser Met Ala Trp Leu Ser Gly Ile Ala Thr Thr
165 170 175
Leu Val Gln Ser Thr Leu Thr Leu Gln Leu Pro Phe Cys Gly His Arg
180 185 190
Gln Val Asp His Phe Ile Cys Glu Val Pro Val Leu Ile Lys Leu Ala
195 200 205
Cys Val Gly Thr Thr Phe Asn Glu Ala Glu Leu Phe Val Ala Ser Ile
210 215 220
Leu Phe Leu Ile Val Pro Val Ser Phe Ile Leu Val Ser Ser Gly Tyr
225 230 235 240
Ile Ala His Ala Val Leu Arg Ile Lys Ser Ala Thr Gly Arg Gln Lys
245 250 255
Ala Phe Gly Thr Cys Phe Ser His Leu Thr Val Val Thr Ile Phe Tyr
260 265 270
Gly Thr Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Arg Ser Arg
275 280 285
Asp Gln Gly Lys Phe Val Ser Leu Phe Tyr Thr Val Val Thr Arg Met
290 295 300
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Ile Lys Glu Val Lys Gly Ala
305 310 315 320
Leu Lys Lys Val Leu Ala Lys Ala Leu Gly Val Asn Ile Leu
325 330

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-1

<400> 9
atgttgggga acgtcgccat c 21

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-1

<400> 10
tcatccacag agcctccaga t 21

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-2

<400> 11
atggaaagg acaatccagt t 21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-2

<400> 12
ctaagagagt aactccagca a 21

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-3

<400> 13			
atggaaatag ccaatgtgag ttc		23	
<210> 14			
<211> 22			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence:PCR			
amplification primer for BCA-GPCR-3			
<400> 14			
taaatttgcg ccagcttgcc tg		22	
<210> 15			
<211> 23			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence:PCR			
amplification primer for BCA-GPCR-4			
<400> 15			
atggtgagac ataccaatga gag		23	
<210> 16			
<211> 24			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence:PCR			
amplification primer for BCA-GPCR-4			
<400> 16			
cataaaatat ttactcccaag agcc		24	
<210> 17			
<211> 1011			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (1)..(1011)			
<223> human breast cancer amplified G-protein coupled			
receptor 3-B (BCA-GPCR-3-B)			
<400> 17			
atg ccc tgt gct ctt ccc aca ggt ggc ctt ttg ccc cac ccc cag cat		48	
Met Pro Cys Ala Leu Pro Thr Gly Gly Leu Leu Pro His Pro Gln His			
1	5	10	15

aca atg atg gaa ata gcc aat gtg agt tct cca gaa gtc ttt gtc ctc	96
Thr Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu	
20 25 30	
ctg ggc ttc tcc gca cga ccc tca cta gaa act gtc ctc ttc ata gtt	144
Leu Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val	
35 40 45	
gtc ttg agt ttt tac atg gta tcg atc ttg ggc aat ggc atc atc att	192
Val Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile	
50 55 60	
ctg gtc tcc cat aca gat gtg cac ctc cac aca cct atg tac ttc ttt	240
Leu Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe	
65 70 75 80	
ctt gcc aac ctc tcc ttc ctg gac atg agc ttc acc acg agc att gtc	288
Leu Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val	
85 90 95	
cca cag ctc ctg gct aac ctc tgg gga cca cag aaa acc ata agc tat	336
Pro Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr	
100 105 110	
gga ggg tgt gtg gtc cag ttc tat atc tcc cat tgg ctg ggg gca acc	384
Gly Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr	
115 120 125	
gag tgt gtc ctg ctg gcc acc atg tcc tat gac cgc tac gct gcc atc	432
Glu Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile	
130 135 140	
tgc agg cca ctc cat tac act gtc att atg cat cca cag ctt tgc ctt	480
Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu	
145 150 155 160	
ggg cta gct ttg gcc tcc tgg ctg ggg ggt ctg acc acc agc atg gtg	528
Gly Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val	
165 170 175	
ggc tcc acg ctc acc atg ctc cta ccg ctg tgt ggg aac aat tgc atc	576
Gly Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile	
180 185 190	
gac cac ttc ttt tgc gag atg ccc ctc att atg caa ctg gct tgt gtg	624
Asp His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val	
195 200 205	
gat acc agc ctc aat gag atg gag atg tac ctg gcc agc ttt gtc ttt	672
Asp Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe	
210 215 220	
gtt gtc ctg cct ctg ggg ctc atc ctg gtc tct tac ggc cac att gcc	720
Val Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala	
225 230 235 240	
cgg gcc gtg ttg aag atc agg tca gca gaa ggg cgg aga aag gca ttc	768
Arg Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe	
245 250 255	

aac acc tgt tct tcc cac gtg gct gtg gtg tct ctg ttt tac ggg agc	816		
Asn Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser			
260	265	270	
atc atc ttc atg tat ctc cag cca gcc aag agc acc tcc cat gag cag	864		
Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln			
275	280	285	
ggc aag ttc ata gct ctg ttc tac acc gta gtc act cct gcg ttg aac	912		
Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn			
290	295	300	
cca ctt att tac acc ctg agg aac acg gag gtg aag agc gcc ctc cgg	960		
Pro Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg			
305	310	315	320
cac atg gta tta gag aac tgc tgt ggc tct gca ggc aag ctg gcg caa	1008		
His Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln			
325	330	335	

att	1011
Ile	

<210> 18
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<223> human breast cancer amplified G-protein coupled
receptor 3-B (BCA-GPCR-3-B)

<400> 18			
Met Pro Cys Ala Leu Pro Thr Gly Gly Leu Leu Pro His Pro Gln His			
1	5	10	15
Thr Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu			
20	25	30	
Leu Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val			
35	40	45	
Val Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile			
50	55	60	
Leu Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe			
65	70	75	80
Leu Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val			
85	90	95	
Pro Gln Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr			
100	105	110	
Gly Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr			
115	120	125	
Glu Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile			
130	135	140	
Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu			
145	150	155	160
Gly Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val			
165	170	175	
Gly Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile			
180	185	190	
Asp His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val			
195	200	205	

Asp Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe
 210 215 220
 Val Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala
 225 230 235 240
 Arg Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe
 245 250 255
 Asn Thr Cys Ser Ser His Val Ala Val Ser Leu Phe Tyr Gly Ser
 260 265 270
 Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln
 275 280 285
 Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn
 290 295 300
 Pro Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg
 305 310 315 320
 His Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
 325 330 335
 Ile

<210> 19
 <211> 960
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(960)
 <223> human breast cancer amplified G-protein coupled
 receptor 3-C (BCA-GPCR-3-C)

<400> 19
 atg atg gaa ata gcc aat gtg agt tct cca gaa gtc ttt gtc ctc ctg 48
 Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
 1 5 10 15
 ggc ttc tcc gca cga ccc tca cta gaa act gtc ctc ttc ata gtt gtc 96
 Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
 20 25 30
 ttg agt ttt tac atg gta tcg atc ttg ggc aat ggc atc atc att ctg 144
 Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu
 35 40 45
 gtc tcc cat aca gat gtg cac ctc cac aca cct atg tac ttc ttt ctt 192
 Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 gcc aac ctc tcc ttc ctg gac atg agc ttc acc acg agc att gtc cca 240
 Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
 65 70 75 80
 cag ctc ctg gct aac ctc tgg gga cca cag aaa acc ata agc tat gga 288
 Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
 85 90 95
 ggg tgt gtg gtc cag ttc tat atc tcc cat tgg ctg ggg gca acc gag 336
 Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
 100 105 110

tgt gtc ctg ctg gcc acc atg tcc tat gac cgc tac gct gcc atc tgc		384	
Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys			
115	120	125	
agg cca ctc cat tac act gtc att atg cat cca cag ctt tgc ctt ggg		432	
Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly			
130	135	140	
cta gct ttg gcc tcc tgg ctg ggg ggt ctg acc acc agc atg gtg ggc		480	
Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly			
145	150	155	160
tcc acg ctc acc atg ctc cta ccg ctg tgt ggg aac aat tgc atc gac		528	
Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp			
165	170	175	
cac ttc ttt tgc gag atg ccc ctc att atg caa ctg gct tgt gtg gat		576	
His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp			
180	185	190	
acc agc ctc aat gag atg gag atg tac ctg gcc agc ttt gtc ttt gtt		624	
Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val			
195	200	205	
gtc ctg cct ctg ggg ctc atc ctg gtc tct tac ggc cac att gcc cg		672	
Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg			
210	215	220	
gcc gtg ttg aag atc agg tca gca gaa ggg cg aga aag gca ttc aac		720	
Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn			
225	230	235	240
acc tgt tct tcc cac gtg gct gtg tct ctg ttt tac ggg agc atc		768	
Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile			
245	250	255	
atc ttc atg tat ctc cag cca gcc aag agc acc tcc cat gag cag ggc		816	
Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly			
260	265	270	
aag ttc ata gct ctg ttc tac acc gta gtc act cct gcg ttg aac cca		864	
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro			
275	280	285	
ctt att tac acc ctg agg aac acg gag gtg aag agc gcc ctc cgg cac		912	
Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His			
290	295	300	
atg gta tta gag aac tgc tgt ggc tct gca ggc aag ctg gcg caa att		960	
Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile			
305	310	315	320

<210> 20
<211> 320
<212> PRT
<213> Homo sapiens

<220>
<223> human breast cancer amplified G-protein coupled receptor 3-C (BCA-GPCR-3-C)

<400> 20
 Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
 1 5 10 15
 Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
 20 25 30
 Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu
 35 40 45
 Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
 65 70 75 80
 Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
 85 90 95
 Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
 100 105 110
 Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly
 130 135 140
 Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly
 145 150 155 160
 Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp
 165 170 175
 His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp
 180 185 190
 Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val
 195 200 205
 Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg
 210 215 220
 Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile
 245 250 255
 Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly
 260 265 270
 Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro
 275 280 285
 Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His
 290 295 300
 Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
 305 310 315 320

<210> 21
<211> 957
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(957)
<223> human breast cancer amplified G-protein coupled
 receptor 3-D (BCA-GPCR-3-D)

<400> 21
 atg gaa ata gcc aat gtg agt tct cca gaa gtc ttt gtc ctc ctg ggc 48
 Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu Gly
 1 5 10 15

ttc tcc gca cga ccc tca cta gaa act gtc ctc ttc ata gtt gtc ttg		96	
Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val Leu			
20	25	30	
agt ttt tac atg gta tcg atc ttg ggc aat ggc atc atc att ctg gtc		144	
Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu Val			
35	40	45	
tcc cat aca gat gtg cac ctc cac aca cct atg tac ttc ttt ctt gcc		192	
Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ala			
50	55	60	
aac ctc tcc ttc ctg gac atg agc ttc acc acg agc att gtc cca cag		240	
Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln			
65	70	75	80
ctc ctg gct aac ctc tgg gga cca cag aaa acc ata agc tat gga ggg		288	
Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly			
85	90	95	
tgt gtg gtc cag ttc tat atc tcc cat tgg ctg ggg gca acc gag tgt		336	
Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys			
100	105	110	
gtc ctg ctg gcc acc atg tcc tat gac cgc tac gct gcc atc tgc agg		384	
Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg			
115	120	125	
cca ctc cat tac act gtc att atg cat cca cag ctt tgc ctt ggg cta		432	
Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly Leu			
130	135	140	
gct ttg gcc tcc tgg ctg ggg ggt ctg acc acc agc atg gtg ggc tcc		480	
Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser			
145	150	155	160
acg ctc acc atg ctc cta ccg ctg tgt ggg aac aat tgc atc gac cac		528	
Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His			
165	170	175	
ttc ttt tgc gag atg ccc ctc att atg caa ctg gct tgt gtg gat acc		576	
Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr			
180	185	190	
agc ctc aat gag atg gag atg tac ctg gcc agc ttt gtc ttt gtt gtc		624	
Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val			
195	200	205	
ctg cct ctg ggg ctc atc ctg gtc tct tac ggc cac att gcc cgg gcc		672	
Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala			
210	215	220	
gtg ttg aag atc agg tca gca gaa ggg cgg aga aag gca ttc aac acc		720	
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr			
225	230	235	240
tgt tct tcc cac gtg gct gtg tct ctg ttt tac ggg agc atc atc		768	
Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile			
245	250	255	

ttc atg tat ctc cag cca gcc aag agc acc tcc cat gag cag ggc aag	816
Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys	
260	265
270	
ttc ata gct ctg ttc tac acc gta gtc act cct gcg ttg aac cca ctt	864
Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu	
275	280
285	
att tac acc ctg agg aac acg gag gtg aag agc gcc ctc cgg cac atg	912
Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His Met	
290	295
295	300
gta tta gag aac tgc tgt ggc tct gca ggc aag ctg gcg caa att	957
Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile	
305	310
310	315

<210> 22

<211> 319

<212> PRT

<213> Homo sapiens

<220>

<223> human breast cancer amplified G-protein coupled receptor 3-D (BCA-GPCR-3-D)

<400> 22

Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu Gly			
1	5	10	15
Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val Leu			
20	25	30	
Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu Val			
35	40	45	
Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ala			
50	55	60	
Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln			
65	70	75	80
Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly			
85	90	95	
Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys			
100	105	110	
Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg			
115	120	125	
Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly Leu			
130	135	140	
Ala Leu Ala Ser Trp Leu Gly Leu Thr Thr Ser Met Val Gly Ser			
145	150	155	160
Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His			
165	170	175	
Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr			
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Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val			
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Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala			
210	215	220	
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr			
225	230	235	240
Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile			
245	250	255	
Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys			
260	265	270	

Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
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